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SEQUENCE LISTING

<110> Unilever PLC
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<120> Antigen-Binding Proteins

<130> 56159-5041

<140> US 09/807,172
<141> 2001-04-10

<150> PCT/EP98/06991
<151> 1998-10-27

<150> EP 99303118.6
<151> 1999-04-22

<150> PCT/EP99/08323
<151> 1999-10-22

<160> 51

<170> PatentIn version 3.1

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1 5

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Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr
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 aggtsmarct gcagsagtcw gg

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 aacagttaag ctccgcttg cggccgcgga gctggggctc tcgctgtggt gcg 53

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 aacagttaag ctccgcttg cggccgcgtg ttgtggtttt ggtgtcttgg gtt 53

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 gggaattcca atagggtggt agcaatcg 28

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 gaccaacgtg gtcgcctggc aaaacg 26

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Ala His His Thr Asn Lys Lys Gln Asn Lys Met Met Leu Leu Gln Ala Phe
 1 5 10 15

Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys Ile Ser Ala Gln Val Gln
 20 25 30

Leu Gln Glu Ser
 35

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Gly Thr Gln Val Thr Val Ser Ser
 1 5

<210> 16

<211> 5

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<223> First 5 codons of HC-V domain

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Gln Val Gln Leu Gln
 1 5

<210> 17

<211> 188

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 tggetggttt tgcagccaaa atatctgcgc aggtgcagct gcaggagtcg taatgaggga 120
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<400> 18

Ala His His Thr Asn Lys Gln Asn Lys Met Met Leu Leu Gln Ala Phe
 1 5 10 15

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 20 25 30

Leu Gln Glu Ser

35

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Gly Thr Gln Val Thr Val Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu
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Asp Leu Asn

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1 5

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gln Leu Val Gln Ala Gly Gly
1 5 10 15
tct ctg aaa ctc tcc tgt gca gcc tct gga aac acc ttc agt ggc ggc 96
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Asn Thr Phe Ser Gly Gly
20 25 30

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ttc atg ggc tgg tac cgc cag gct cca ggg aag cag cgc gag ttg gtc      144
Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
      35              40              45

gca acc att aat agt aga ggt atc aca aac tat gca gac ttc gtg aag      192
Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val Lys
      50              55              60

ggc cga ttc acc atc tcc aga gac aat gcc aag aag aca gtg tat ttg      240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu
      65              70              75              80

gaa atg aac agc ctg gaa cct gaa gac acg gcc gtt tat tac tgt tac      288
Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Tyr
      85              90              95

act cac tac ttc aga tcc tac tgg ggt cag ggg acc cag gtc acc gtc      336
Thr His Tyr Phe Arg Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
      100             105             110

tcc tca      342
Ser Ser

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<210> 22
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<400> 22

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Glu
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Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Asn Thr Phe Ser Gly Gly
      20              25              30

Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
      35              40              45

Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val Lys
      50              55              60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu
      65              70              75              80

Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Tyr
      85              90              95

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Thr His Tyr Phe Arg Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
 100 105 110

Ser Ser

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 tct ctg aga ctc tcc tgt gca gcc tct gga cgc acc gcc agt acg tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr
 20 25 30
 gac atg ggc tgg ttc cgc cag gct cca ggg aag gag cgt gag tct gta 144
 Asp Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val
 35 40 45
 gca gct att aac tgg gat agt gcg cgc aca tac tat gca agc tcc gtg 192
 Ala Ala Ile Asn Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val
 50 55 60
 agg ggc cga ttc acc atc tcc aga gac aac gcc aag aag acg gtg tat 240
 Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
 65 70 75 80
 ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt tat acc tgt 288
 Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys
 85 90 95
 ggc gcg ggg gaa ggt ggt act tgg gac tcc tgg ggc cag ggg acc cag 336
 Gly Ala Gly Glu Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln
 100 105 110
 gtc acc gtc tcc tca 351
 Val Thr Val Ser Ser
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<400> 24

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr
 20 25 30

Asp Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val
 35 40 45

Ala Ala Ile Asn Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val
 50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys
 85 90 95

Gly Ala Gly Glu Gly Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln
 100 105 110

Val Thr Val Ser Ser
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<400> 25
 gaattaagcg gccgcccgag tgaaactgct cgagtcwggg gga

43

<210> 26
 <211> 42
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<213> Artificial sequence

<220>

<223> Primer

<400> 26

ccctgggtcc agtggcagag gagtggcaga ggagtcttgt tt

42

<210> 27

<211> 24

<212> DNA

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<220>

<223> Primer

<400> 27

caggtccagc tgcaggagtc tggg

24

<210> 28

<211> 24

<212> DNA

<213> Artificial sequence

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<400> 28

caggtgaaac tgctcgagtc wggg

24

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<211> 55

<212> DNA

<213> Artificial sequence

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<223> Linker; Double stranded

<220>

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<222> (2)..(40)

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50

1

5

10

agctt

55

<210> 30

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<400> 30

Val Thr Val Ser Ser Gln Val Gln Leu Gln Glu Ser Leu

1

5

10

<210> 31

<211> 8

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<400> 31

Gln Val Gln Leu Gln Glu Ser Gly

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<211> 672

<212> DNA

<213> Artificial sequence

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<222> (1)..(672)

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Leu Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu

1

5

10

15

tcc tgt gca gcc tct gga cgc acc ggc agt acg tat gac atg ggc tgg 96

Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr Asp Met Gly Trp

20

25

30

ttc cgc cag gct cca ggg aag gag cgt gag tct gta gca gct att aac 144

Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val Ala Ala Ile Asn

35

40

45

tgg gat agt gcg cgc aca tac tat gca agc tcc gtg agg ggc cga ttc 192

Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val Arg Gly Arg Phe

50

55

60

acc atc tcc aga gac aac gcc aag acg gtg tat ctg caa atg aac 240

Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu Gln Met Asn

65	70	75	80	
agc ctg aaa cct gag gac acg gcc gtt tat acc tgt ggc gcg ggg gaa				288
Ser Leu Lys Pro	Glu Asp Thr Ala Val Tyr	Thr Cys Gly Ala Gly	Glu	
	85	90	95	
ggg ggt act tgg gac tcc tgg ggc cag ggg acc cag gtc acc gtc tcc				336
Gly Gly Thr Trp Asp Ser Trp	Gly Gln Gly Thr	Gln Val Thr	Val Ser	
	100	105	110	
tca cag gtg cag ctg cag gag tca ggg gga ggc ttg gtg cag gct ggg				384
Ser Gln Val Gln Leu Gln Glu Ser	Gly Gly Gly Leu Val Gln Ala Gly			
	115	120	125	
gag tct ctg aaa ctc tcc tgt gca gcc tct gga aac acc ttc agt ggc				432
Glu Ser Leu Lys Leu Ser Cys Ala Ala Ser	Gly Asn Thr Phe Ser Gly			
	130	135	140	
ggc ttc atg ggc tgg tac cgc cag gct cca ggg aag cag cgc gag ttg				480
Gly Phe Met Gly Trp Tyr Arg Gln Ala Pro	Gly Lys Gln Arg Glu Leu			
	145	150	155	160
gtc gca acc att aat agt aga ggt atc aca aac tat gca gac ttc gtg				528
Val Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val				
	165	170	175	
aag ggc cga ttc acc atc tcc aga gac aat gcc aag aag aca gtg tat				576
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr				
	180	185	190	
ttg gaa atg aac agc ctg gaa cct gaa gac acg gcc gtt tat tac tgt				624
Leu Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys				
	195	200	205	
tac act cac tac ttc aga tcc tac tgg ggt cag ggg acc cag gtc acc				672
Tyr Thr His Tyr Phe Arg Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr				
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<400> 33				
Leu Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu				
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Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr Asp Met Gly Trp				
	20	25	30	

Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val Ala Ala Ile Asn
 35 40 45

Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val Arg Gly Arg Phe
 50 55 60

Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu Gln Met Asn
 65 70 75 80

Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys Gly Ala Gly Glu
 85 90 95

Gly Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 100 105 110

Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly
 115 120 125

Glu Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Asn Thr Phe Ser Gly
 130 135 140

Gly Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu
 145 150 155 160

Val Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val
 165 170 175

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
 180 185 190

Leu Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 195 200 205

Tyr Thr His Tyr Phe Arg Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr
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48

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 <211> 47
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 <213> Artificial sequence

<220>
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<400> 36
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23

<210> 37
 <211> 16
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<400> 37
 accatgaagg ccaagg

16

<210> 38
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<400> 38
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35

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<220>

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aagaagtaga cgaagacgga gaagtcgg

28

<210> 40

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<212> DNA

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<223> Linker

<400> 40

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29

<210> 41

<211> 22

<212> DNA

<213> Artificial sequence

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<223> Linker

<400> 41

accaagaggt ccaagtgggtc ca

22

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ctagtgtctac tacaactggt tcttcaccag gtccaactca g

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<210> 43

<211> 34

<212> DNA

<213> Artificial sequence

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<223> Linker

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acgatgatgt tgaccaagaa gtggtcagg ttga

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<211> 32

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<400> 44

ctagtgtctaa tcattctgggt aatgcttctc ag

32

<210> 45

<211> 25

<212> DNA

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acgattagta agaccattac gaaga

25

<210> 46

<211> 8

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<223> Primer

<400> 46

Gln Val Lys Leu Leu Glu Ser Gly

1 5

<210> 47

<211> 7

<212> PRT

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<400> 47

Ser Gly Thr Ser Gly Ser Gln

1 5

<210> 48

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<400> 48

Ser Ser Ser Ser Ala Ser Ala Ser Ser Ala Gln
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<211> 9

<212> PRT

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<400> 49

Ser Gly Ser Pro Gly Ser Pro Gly Gln
1 5

<210> 50

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Ser Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
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<210> 51

<211> 10

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